

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Beaudry, Gary A.
Maddon, Paul J.
- (ii) TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.24
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/485,163
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
- (viii) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: homo sapien
(G) CELL TYPE: lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Applicants : Gary Beaudry and
Paul J. Maddon
Serial No. : 08/485,163
Filed : June 7, 1995
Exhibit A

Phe Glu Arg Lys Cys Cys Val Gln Cys Pro Pro Cys Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (G) CELL TYPE: Lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAAGCCCAGA GCCCTGCCAT TTCTGTGGGC TCAGGTCCTT ACTGCTCAGC CCCTTCCTCC 60
CTCGGCAAGG CCACAATGAA CCGGGGAGTC CCTTTTAGGC ACTTGCTTCT GGTGCTGCAA 120
CTGGCGCTCC TCCCAGCAGC CACTCAGGGA AAGAAAGTGG TGCTGGGCAA AAAAGGGGAT 180
ACAGTGGAAC TGACCTGTAC AGCTTCCCAG AAGAAGAGCA TACAATTCCA CTGAAAAAAC 240
TCCAACCAGA TAAAGATTCT GGGAAATCAG GGCTCCTTCT TAACTAAAGG TCCATCCAAG 300
CTGAATGATC GCGCTGACTC AAGAAGAAGC CTTTGGGACC AAGGAAACTT CCCCCTGATC 360
ATCAAGAATC TTAAGATAGA AGACTCAGAT ACTTACATCT GTGAAGTGGA GGACCAGAAG 420
GAGGAGGTGC AATTGCTAGT GTTCGGATTG ACTGCCAACT CTGACACCCA CCTGCTTCAG 480
GGGCAGAGCC TGACCCTGAC CTTGGAGAGC CCCCCTGGTA GTAGCCCCTC AGTGCAATGT 540
AGGAGTCCAA GGGGTAAAAA CATACAGGGG GGAAGACCC TCTCCGTGTC TCAGCTGGAG 600
CTCCAGGATA GTGGCACCTG GACATGCACT GTCTTGCGAG ACCAGAAGAA GGTGGAGTTC 660
AAAATAGACA TCGTGGTGCT AGCTTTCGAG CGCAAATGTT GTGTCGAGTG CCCACCGTGC 720
CCAGGTAAGC CAGCCCAGGC CTCGCCCTCC AGCTCAAGGC GGGACAGGTG CCCTAGAGTA 780
GCCTGCATCC AGGGACAGGC CCCAGCTGGG TGCTGACACG TCCACCTCCA TCTCTTCCTC 840
AGCACCACCT GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CCAAACCCA AGGACACCCT 900
CATGATCTCC CGGACCCCTG AGGTCACGTG CGTGGTGGTG GACGTGAGCC ACGAAGACCC 960
CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG CATAATGCCA AGACAAAGCC 1020
ACGGGAGGAG CAGTTCAACA GCACGTTCCG TGTGGTCAGC GTCCTCACCG TTGTGCACCA 1080
GGACTGGCTG AACGGCAAGG AGTACAAGTG CAAGGTCTCC AACAAAGGCC TCCCAGCCCC 1140

E1
Cont

CATCGAGAAA ACCATCTCCA AAACCAAAGG TGGGACCCGC GGGGTATGAG GGCCACATGG	1200
ACAGAGGCCG GCTCGGCCCA CCCTCTGCCC TGGGAGTGAC CGCTGTGCCA ACCTCTGTCC	1260
CTACAGGGCA GCCCCGAGAA CCACAGGTGT ACACCCTGCC CCCATCCCGG GAGGAGATGA	1320
CCAAGAACCA GGTCAGCCTG ACCTGCCTGG TCAAAGGCTT CTACCCCAGC GACATCGCCG	1380
TGGAGTGGGA GAGCAATGGG CAGCCGGAGA ACAACTACAA GACCACACCT CCCATGCTGG	1440
ACTCCGACGG CTCCTTCTTC CTCTACAGCA AGCTCACCGT GGACAAGAGC AGGTGGCAGC	1500
AGGGGAACTG CTTCTCATGC TCCGTGATGC ATGAGGCTCT GCACAACCAC TACACGCAGA	1560
AGAGCCTCTC CCTGTCTCCG GGTAATGAG TGCCACGGCC GGCAAGCCCC CGCTCCCCAG	1620
GCTCTCGGGG TCGCGTGAGG ATGCTTGGCA CGTACCCCGT GTACATACTT CCCAGGCACC	1680
CAGCATGGAA ATAAAGCACC CAGCGCTGCC CTGGGCCCCCT GCGAGACTGT GATGGTTCTT	1740
TCCGTGGGTC AGGCCGAGTC TGAGGCCTGA GTGGCATGAG GGAGGCAGAG TGGGTC	1796

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homo sapien
 - (G) CELL TYPE: lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
1 5 10 15

Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
20 25 30

Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
35 40 45

Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
50 55 60

Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65 70 75 80

E'
Cont.

Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile	
				85					90					95		
Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu	
			100					105					110			
Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn	
		115					120					125				
Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu	
	130					135					140					
Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly	
145					150					155					160	
Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu	
			165						170					175		
Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys	
			180					185					190			
Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Glu	Arg	Lys	Cys	
		195					200					205				
Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	
	210					215					220					
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	
225					230					235					240	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	
				245					250					255		
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	
			260					265					270			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	
		275					280					285				
Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	
	290					295					300					
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	
305					310					315					320	

E!
cont

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
325 330 335

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
340 345 350

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
355 360 365

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
370 375 380

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
385 390 395 400

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
405 410 415

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
420 425 430

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapien
- (G) CELL TYPE: lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAAGCCCAGA GCCCTGCCAT TTCTGTGGGC TCAGGTCCCT ACTGCTCAGC CCCTTCCTCC	60
CTCGGCAAGG CCACAATGAA CCGGGGAGTC CCTTTTAGGC ACTTGCTTCT GGTGCTGCAA	120
CTGGCGCTCC TCCCAGCAGC CACTCAGGGA AAGAAAGTGG TGCTGGGCAA AAAAGGGGAT	180
ACAGTGGAAAC TGACCTGTAC AGCTTCCCAG AAGAAGAGCA TACAATTCCA CTGGAAAAAC	240
TCCAACCAGA TAAAGATTCT GGGAAATCAG GGCTCCTTCT TAACTAAAGG TCCATCCAAG	300
CTGAATGATC GCGCTGACTC AAGAAGAAGC CTTTGGGACC AAGGAAACTT CCCCCTGATC	360

E1
cont.

ATCAAGAATC	TTAAGATAGA	AGACTCAGAT	ACTTACATCT	GTGAAGTGGA	GGACCAGAAG	420
GAGGAGGTGC	AATTGCTAGT	GTTCGGATTG	ACTGCCAACT	CTGACACCCA	CCTGCTTCAG	480
GGGCAGAGCC	TGACCCTGAC	CTTGGAGAGC	CCCCCTGGTA	GTAGCCCCTC	AGTGCAATGT	540
AGGAGTCCAA	GGGGTAAAAA	CATACAGGGG	GGGAAGACCC	TCTCCGTGTC	TCAGCTGGAG	600
CTCCAGGATA	GTGGCACCTG	GACATGCACT	GTCTTGACAG	ACCAGAAGAA	GGTGGAGTTC	660
AAAATAGACA	TCGTGGTGCT	AGCTTTCGCC	TCCACCAAGG	GCCCATCGGT	CTTCCCCCTG	720
GCGCCCTGCT	CCAGGAGCAC	CTCCGAGAGC	ACAGCCGCCC	TGGGCTGCCT	GGTCAAGGAC	780
TACTTCCCCG	AACCGGTGAC	GGTGTGCTGG	AACTCAGGCG	CTCTGACCAG	CGGCGTGCAC	840
ACCTTCCCAG	CTGTCCTACA	GTCTCAGGA	CTCTACTCCC	TCAGCAGCGT	GGTGACCGTG	900
CCCTCCAGCA	ACTTCGGCAC	CCAGACCTAC	ACCTGCAACG	TAGATCACAA	GCCCAGCAAC	960
ACCAAGGTGG	ACAAGACAGT	TGGTGAGAGG	CCAGCTCAGG	GAGGGAGGGT	GTCTGCTGGA	1020
AGCCAGGCTC	AGCCCTCCTG	CCTGGACGCA	CCCCGGCTGT	GCAGCCCCAG	CCCAGGGCAG	1080
CAAGGCAGGC	CCCATCTGTC	TCCTCACCCG	GAGGCCTCTG	CCCGCCCCAC	TCATGCTCAG	1140
GGAGAGGGTC	TTCTGGCTTT	TTCCACCAGG	CTCCAGGCAG	GCACAGGCTG	GGTGCCCTTA	1200
CCCCAGGCCC	TTCACACACA	GGGGCAGGTG	CTTGGCTCAG	ACCTGCCAAA	AGCCATATCC	1260
GGGAGGACCC	TGCCCCTGAC	CTAAGCCGAC	CCCAAAGGCC	AACTGTCCA	CTCCCTCAGC	1320
TCGGACACCT	TCTCTCCTCC	CAGATCCGAG	TAActCCCAA	TCTTCTCTCT	GCAGAGCGCA	1380
AATGTTGTGT	CGAGTGCCCA	CCGTGCCCAG	GTAAGCCAGC	CCAGGCCTCG	CCCTCCAGCT	1440
CAAGGCGGGA	CAGGTGCCCT	AGAGTAGCCT	GCATCCAGGG	ACAGGCCCCA	GCTGGGTGCT	1500
GACACGTCCA	CCTCCATCTC	TTCCTCAGCA	CCACCTGTGG	CAGGACCGTC	AGTCTTCCTC	1560
TTCCCCCCTA	AACCCAAGGA	CACCCTCATG	ATCTCCCGGA	CCCCTGAGGT	CACGTGCGTG	1620
GTGGTGGACG	TGAGCCACGA	AGACCCGAG	GTCCAGTTCA	ACTGGTACGT	GGACGGCGTG	1680
GAGGTGCATA	ATGCCAAGAC	AAAGCCACGG	GAGGAGCAGT	TCAACAGCAC	GTTCCGTGTG	1740
GTCAGCGTCC	TCACCGTTGT	GCACCAGGAC	TGGCTGAACG	GCAAGGAGTA	CAAGTGCAAG	1800
GTCTCCAACA	AAGGCCTCCC	AGCCCCCATC	GAGAAAACCA	TCTCCAAAAC	CAAAGGTGGG	1860
ACCCGCGGGG	TATGAGGGCC	ACATGGACAG	AGGCCGGCTC	GGCCCACCCT	CTGCCCTGGG	1920
AGTGACCGCT	GTGCCAACCT	CTGTCCCTAC	AGGGCAGCCC	CGAGAACCAC	AGGTGTACAC	1980
CCTGCCCCCA	TCCCGGGAGG	AGATGACCAA	GAACCAGGTC	AGCCTGACCT	GCCTGGTCAA	2040
AGGCTTCTAC	CCCAGCGACA	TCGCCGTGGA	GTGGGAGAGC	AATGGGCAGC	CGGAGAACAA	2100

E
cont

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CTACAAGACC ACACCTCCCA TGCTGGACTC CGACGGCTCC TTCTTCCTCT ACAGCAAGCT 2160
CACCGTGGAC AAGAGCAGGT GGCAGCAGGG GAACGTCTTC TCATGCTCCG TGATGCATGA 2220
GGCTCTGCAC AACCACTACA CGCAGAAGAG CCTCTCCCTG TCTCCGGGTA AATGAGTGCC 2280
ACGGCCGGCA AGCCCCCGCT CCCCAGGCTC TCGGGGTCGC GTGAGGATGC TTGGCACGTA 2340
CCCCGTGTAC ATACTTCCCA GGCACCCAGC ATGGAAATAA AGCACCCAGC GCTGCCCTGG 2400
GCCCCTGCGA GACTGTGATG GTTCTTTCCG TGGGTCAGGC CGAGTCTGAG GCCTGAGTGG 2460
CATGAGGGAG GCAGAGTGGG TC 2482

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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 530 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapien
- (G) CELL TYPE: lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
1           5           10           15

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Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
20           25           30

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Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
35           40           45

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Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
50           55           60

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Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65           70           75           80

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Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
85           90           95

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E1
Cont

Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu
		100						105					110		
Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn
		115					120					125			
Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu
	130					135					140				
Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly
145					150					155					160
Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu
				165					170					175	
Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys
			180					185					190		
Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Ala	Ser	Thr	Lys
		195					200					205			
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu
	210					215					220				
Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro
225					230					235					240
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr
				245					250					255	
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
			260					265					270		
Val	Thr	Val	Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn
		275					280					285			
Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Arg
	290					295					300				
Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly
305					310					315					320
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
				325					330					335	

E1
cont.

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
340 345 350

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
355 360 365

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
370 375 380

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
385 390 395 400

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
405 410 415

Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
420 425 430

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
435 440 445

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
450 455 460

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
465 470 475 480

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
485 490 495

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
500 505 510

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
515 520 525

Gly Lys
530

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA

E1
cont

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homo sapien
(G) CELL TYPE: lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAAGCCCAGA GCCCTGCCAT TTCTGTGGGC TCAGGTCCCT ACTGCTCAGC CCCTTCCTCC 60
CTCGGCAAGG CCACAATGAA CCGGGGAGTC CCTTTTAGGC ACTTGCTTCT GGTGCTGCAA 120
CTGGCGCTCC TCCCAGCAGC CACTCAGGGA AAGAAAGTGG TGCTGGGCAA AAAAGGGGAT 180
ACAGTGGAAC TGACCTGTAC AGCTTCCCAG AAGAAGAGCA TACAATTCCA CTGGAAAAAC 240
TCCAACCAGA TAAAGATTCT GGGAAATCAG GGCTCCTTCT TAACTAAAGG TCCATCCAAG 300
CTGAATGATC GCGCTGACTC AAGAAGAAGC CTTTGGGACC AAGGAAACTT CCCCCTGATC 360
ATCAAGAATC TTAAGATAGA AGACTCAGAT ACTTACATCT GTGAAGTGGA GGACCAGAAG 420
GAGGAGGTGC AATTGCTAGT GTTCGGATTG ACTGCCAACT CTGACACCCA CCTGCTTCAG 480
GGGCAGAGCC TGACCCTGAC CTTGGAGAGC CCCCCTGGTA GTAGCCCCTC AGTGCAATGT 540
AGGAGTCCAA GGGGTAAAAA CATACAGGGG GGAAGACCC TCTCCGTGTC TCAGCTGGAG 600
CTCCAGGATA GTGGCACCTG GACATGCACT GTCTTGCAAG ACCAGAAGAA GGTGGAGTTC 660
AAAATAGACA TCGTGGTGCT AGCTTTTCACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 720
CCATCTGATG AGCAGTTGAA ATCTGGAACCT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 780
TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 840
CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTG 900
ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 960
GGCCTGAGCT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGTTAGAG GGAGAAGTGC 1020
CCCCACCTGC TCCTCAGTTC CAGCCTGACC CCCTCCCATC CTTTGGCCTC TGACCCTTTT 1080
TCCACAGGGG ACCTACCCCT ATTGCGGTCC TCCAAGCTCA TCTTTCACCT CACCCCCCTC 1140
CTCCTCCTT 1149

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

1
E
Cont

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homo sapien
(G) CELL TYPE: lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Asn	Arg	Gly	Val	Pro	Phe	Arg	His	Leu	Leu	Leu	Val	Leu	Gln	Leu	1	5	10	15
Ala	Leu	Leu	Pro	Ala	Ala	Thr	Gln	Gly	Lys	Lys	Val	Val	Leu	Gly	Lys	20	25	30	
Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser	35	40	45	
Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn	50	55	60	
Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala	65	70	75	80
Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile	85	90	95	
Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu	100	105	110	
Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn	115	120	125	
Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu	130	135	140	
Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly	145	150	155	160
Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu	165	170	175	
Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys	180	185	190	
Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Thr	Val	Ala	Ala	195	200	205	

E
Cont

Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
210						215					220				
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
225					230					235					240
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
				245					250					255	
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
			260					265					270		
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr
		275					280					285			
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser
	290					295					300				
Phe	Asn	Arg	Gly	Glu	Cys										
305					310										

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: synthetic DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
 - (G) CELL TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACACAACAT TTGCGCTCGA AAGCTAGCAC CACG

34

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

*E-1
cont*

(ii) MOLECULE TYPE: synthetic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(G) CELL TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGCCCTTGG TGGAGGCGAA AGCTAGCACC ACG

33

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: synthetic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(G) CELL TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATGGTGCAG CCACAGTGAA AGCTAGCACC ACG

33

E1
cont

